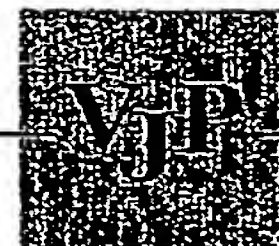


10/583785

VIERING, JENTSCHURA & PARTNER



Dr md

19 JUN 2005

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Ihr Zeichen/Your ref.:

Unser Zeichen/Our file:
P23795

Bearbeiter:
Sd/Ws

Datum/Date:
18.03.2004

International Patent Application PCT/EP03/14542
"Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use"
Appl.: Prof. Dr. Werner Seeger

In reply to the Communication dated February 20, 2004,

an amended sequence listing is filed herewith in written form as well as in computer-readable form (ASCII format; file name: 23795_seq.txt) saved on the enclosed diskette.

The amended sequence listing does not go beyond the disclosure in the application as filed. It now includes the pure amino acid sequences of SEQ ID NOs 1 to 13, which are referred to as SEQ ID NOs 14 to 26, respectively.

Encl.
Sequence listing, paper copy
Diskette

Hans-Martin Viering
Patentanwalt

BEST AVAILABLE COPY

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E-Mail: vjp-la@vjp.de

10/583785

AP20 Rec'd PCT/PTO 19 JUN 2006

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger
 <120> Novel chimeric plasminogen activators and their pharmaceutical use
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 <213> Homo sapiens

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 <223> Coding sequence of the surfactant protein B precursor

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ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
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Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
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Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
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Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
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ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
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Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275 280 285	
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290 295 300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala	
305 310 315 320	
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag	1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys	
325 330 335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg	1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg	
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ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc	1104
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr	
355 360 365	
atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt	1143
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<210> 2
 <211> 837
 <212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag 672
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
 210 215 220

ggc gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg 720
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
 225 230 235 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc 768
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
 245 250 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc 816
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
 260 265 270

ctc gtc ctc cgg tgc tcc atg 837
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<210> 3
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 <213> Homo sapiens

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cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc 96
 Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
 20 25 30

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc 144
 Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
 35 40 45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc 192
 Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
 50 55 60

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg 237
 Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
 65 70 75

<210> 4
 <211> 1293

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

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1 5 10 15	
gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac	96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp	
20 25 30	
tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att	144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile	
35 40 45	
cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata	192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile	
50 55 60	
gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga	240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly	
65 70 75 80	
aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct	288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser	
85 90 95	
gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt	336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu	
100 105 110	
cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg	384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg	
115 120 125	
agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	
gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624

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	225				230					235					240	
cgc	tca	agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	768
Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	
				245					250					255		
gaa	aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	816
Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	
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cac	aac	gac	att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	864
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caa	ggc	cgc	atg	act	ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	1200
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	
	385				390					395				400		
gcc	ctg	aag	gac	aag	cca	ggc	gtc	tac	acg	aga	gtc	tca	cac	ttc	tta	1248
Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	
				405				410						415		
ccc	tgg	atc	cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc		1293
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 <212> DNA
 <213> Homo sapiens

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 <222> (1) ... (828)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

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1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576

Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln		
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Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala		
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gac	cca	cag	tgg	aaa	aca	gat	tcc	tgc	cag	gga	gac	tca	ggg	gga	ccc		672
Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro		
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Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser		
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Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg		
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gtc	tca	cac	ttc	tta	ccc	tgg	atc	cgc	agt	cac	acc	aag	gaa	gag	aat		816
Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn		
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ggc	ctg	gcc	ctc														828
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<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>

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<222> (844) ... (1671)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 6

atg	gct	gag	tca	cac	ctg	ctg	cag	tgg	ctg	ctg	ctg	ctg	ctg	ccc	acg		48
Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr		
1				5				10						15			

ctc	tgt	ggc	cca	ggc	act	gct	gcc	tgg	acc	acc	tca	tcc	ttg	gcc	tgt		96
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys		
			20					25					30				

gcc	cag	ggc	cct	gag	ttc	tgg	tgc	caa	agc	ctg	gag	caa	gca	ttg	cag		144
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln		
		35					40					45					

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly 50 55 60	192
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn 65 70 75 80	240
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu 85 90 95	288
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys 100 105 110	336
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln 115 120 125	384
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys 130 135 140	432
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu 145 150 155 160	480
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu 165 170 175	528
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His 180 185 190	576
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys 195 200 205	624
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys 210 215 220	672
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu 225 230 235 240	720
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile 245 250 255	768
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg 260 265 270	816
ctc gtc ctc cgg tgc tcc atg aag ctt aag ccc tcc tct cct cca gaa Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu 275 280 285	864

gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys 290 295 300	912
att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala 305 310 315 320	960
gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly 325 330 335	1008
ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe 340 345 350	1056
att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser 355 360 365	1104
agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn 370 375 380	1152
ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn 385 390 395 400	1200
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln 405 410 415	1248
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp 420 425 430	1296
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn 435 440 445	1344
tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys 450 455 460	1392
ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu 465 470 475 480	1440
gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp 485 490 495	1488
tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly 500 505 510	1536
cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu	1584

515	520	525	
aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg			1632
Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp			
530	535	540	

atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc	1671
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	
545	550
	555

<210> 7
 <211> 1674
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) ... (837)
 <223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> CDS
 <222> (847) ... (1674)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 7

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1	5
	10
	15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
	20
	25
	30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
	35
	40
	45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50	55
	60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65	70
	75
	80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
	85
	90
	95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
	100
	105
	110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
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Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln		
		115					120					125					
aac	cag	act	gac	tca	aac	ggc	atc	tgt	atg	cac	ctg	ggc	ctg	tgc	aaa		432
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys		
		130				135					140						
tcc	cgg	cag	cca	gag	cca	gag	cag	gag	cca	ggg	atg	tca	gac	ccc	ctg		480
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu		
		145				150				155					160		
ccc	aaa	cct	ctg	cgg	gac	cct	ctg	cca	gac	cct	ctg	ctg	gac	aag	ctc		528
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu		
				165				170						175			
gtc	ctc	cct	gtg	ctg	ccc	ggg	gcc	ctc	cag	gcg	agg	cct	ggg	cct	cac		576
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His		
			180					185					190				
aca	cag	gat	ctc	tcc	gag	cag	caa	ttc	ccc	att	cct	ctc	ccc	tat	tgc		624
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys		
		195					200					205					
tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	ccc	aag		672
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys		
		210				215					220						
ggt	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	cct	ctg		720
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu		
		225				230				235					240		
gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	atc		768
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile		
				245				250						255			
ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	cgc		816
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg		
			260					265					270				
ctc	gtc	ctc	cgg	tgc	tcc	atg	cag	ata	tct	aag	ccc	tcc	tct	cct	cca		864
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro		
			275				280					285					
gaa	gaa	tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt		912
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe		
		290				295					300						
aag	att	att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt		960
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe		
		305				310				315					320		
gcg	gcc	atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt		1008
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys		
				325				330						335			
gga	ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc		1056
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys		
			340					345					350				

ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg 355 360 365	1104
tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu 370 375 380	1152
aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His 385 390 395 400	1200
aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala 405 410 415	1248
cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn 420 425 430	1296
gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu 435 440 445	1344
aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val 450 455 460	1392
aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser 465 470 475 480	1440
gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr 485 490 495	1488
gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500 505 510	1536
ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515 520 525	1584
ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530 535 540	1632
tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545 550 555	1674

<210> 8
 <211> 591
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (591)

<223> Coding sequence of the surfactant protein C precursor

<400> 8

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac	192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	
50 55 60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa	240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	
65 70 75 80	
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc	288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	
85 90 95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc	336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	
100 105 110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca	384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	
115 120 125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc	432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	
130 135 140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag	480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	
145 150 155 160	
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg	528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	
165 170 175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg	576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	
180 185 190	
ccg ctc tac tac atc	591
Pro Leu Tyr Tyr Ile	
195	

<210> 9
<211> 174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (174)
<223> Coding sequence of the surfactant protein C precursor lacking the C-terminal propeptide

<400> 9

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc	174
Val Ile Val Gly Ala Leu Leu Met Gly Leu	
50 55	

<210> 10
<211> 105
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (105)
<223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val	
1 5 10 15	
gtg gtg gtg gtg gtc ctc atc gtc gtg gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu	
20 25 30	
atg ggt ctc	105
Met Gly Leu	
35	

<210> 11
<211> 1686
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1686)

<223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gca gtc ttc gtt tgc ccc agc cag gaa atc cat gcc cga ttc aga aga	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg	144
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met	
35 40 45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac	192
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn	
50 55 60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca	240
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser	
65 70 75 80	
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc	288
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr	
85 90 95	
tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa	336
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu	
100 105 110	
gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac	384
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr	
115 120 125	
gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt	432
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser	
130 135 140	
ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc	480
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro	
145 150 160 165	
tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac	528
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His	
170 175 180	
aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc	576
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val	
185 190 195	
ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc	624
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys	
200 205 205	

tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg 210 215 220	672
ggc acg cac agc ctc acc gag tcg ggt gcc tcc tgc ctc ccg tgg aat Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn 225 230 235 240	720
tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala 245 250 255	768
cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly 260 265 270	816
gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp 275 280 285	864
gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr 290 295 300	912
agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala 305 310 315 320	960
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro 325 330 335	1008
gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile 340 345 350	1056
ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu 355 360 365	1104
acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu 370 375 380	1152
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp 385 390 395 400	1200
gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser 405 410 415	1248
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro 420 425 430	1296
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly	1344

435	440	445	
tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag			1392
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys			
450	455	460	
gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat			1440
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His			
465	470	475	480
tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act			1488
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr			
	485	490	495
cgg agc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat			1536
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp			
	500	505	510
tcg gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg			1584
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val			
	515	520	525
ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt			1632
Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly			
530	535	540	
gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg			1680
Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met			
545	550	555	560
cga ccg			1686
Arg Pro			

<210> 12
 <211> 1158
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> sig_peptide
 <222> (1) ... (69)
 <223> Signal sequence of the surfactant protein B

<220>
 <221> CDS
 <222> (76) ... (312)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> CDS
 <222> (313) ... (1140)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> CDS
 <222> (1141) ... (1158)
 <223> Hexahistidin affinity tag

<400> 12

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr	
20 25 30	
tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc	144
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro	
35 40 45	
aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct	192
Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro	
50 55 60	
ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc	240
Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val	
65 70 75 80	
atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc	288
Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys	
85 90 95	
cgc ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa	336
Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu	
100 105 110	
tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att	384
Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile	
115 120 125	
att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc	432
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala	
130 135 140	
atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc	480
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly	
145 150 155 160	
agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att	528
Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile	
165 170 175	
gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg	576
Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg	
180 185 190	
ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc	624
Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu	
195 200 205	
atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac	672
Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp	
210 215 220	

att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca 720
Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro
225 230 235 240

tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc 768
Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
245 250 255

cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct 816
Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
260 265 270

acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg 864
Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
275 280 285

att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc 912
Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
290 295 300

acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc 960
Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
305 310 315 320

tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc 1008
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
325 330 335

atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag 1056
Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
340 345 350

gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc 1104
Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
355 360 365

cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat 1152
Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
370 375 380

cat cat 1158
His His
385

<210> 13

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<221> sig_peptide

<222> (1) ... (60)

<223> Signal sequence of the urokinase plasminogen activator

<220>

<221> CDS

<222> (67) ... (894)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> CDS

<222> (895) ... (1131)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> CDS

<222> (1132) ... (1149)

<223> Hexahistidin affinity tag

<400> 13

atg	aga	gcc	ctg	ctg	gcg	cgc	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc	48
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser	
1			5					10					15			

gac	tcc	aaa	ggc	agc	aat	aag	ccc	tcc	tct	cct	cca	gaa	gaa	tta	aaa	96
Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	
		20					25					30				

ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag	att	att	ggg	144
Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	
	35					40					45					

gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg	gcc	atc	tac	192
Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	
	50					55				60						

agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga	ggc	agc	ctc	240
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	
65				70				75						80		

atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc	att	gat	tac	288
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	
			85					90						95		

cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggg	cgc	tca	agg	ctt	aac	336
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	
			100					105						110		

tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac	ctc	atc	cta	384
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	
	115					120					125					

cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	aac	gac	att	gcc	432
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	
	130				135					140						

ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	tcc	cgg	480
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	
145				150				155							160	

act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	gat	ccc	cag	ttt	528
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	
			165					170						175		

ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac	576
Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp	
180 185 190	
tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc	624
Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser	
195 200 205	
cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc	672
His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr	
210 215 220	
aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc tgc cag	720
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln	
225 230 235 240	
gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act	768
Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr	
245 250 255	
ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag	816
Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys	
260 265 270	
cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt	864
Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser	
275 280 285	
cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc	912
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro	
290 295 300	
tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att	960
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile	
305 310 315 320	
ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta	1008
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val	
325 330 335	
cct ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc	1056
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser	
340 345 350	
gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc	1104
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val	
355 360 365	
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
370 375 380	

<210> 14

<211> 381

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (381)

<223> Surfactant protein B precursor

<400> 14

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr
1				5				10						15	
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys
			20					25					30		
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln
		35					40					45			
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly
	50					55					60				
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn
65					70					75					80
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu
			85						90					95	
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys
			100					105					110		
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln
		115					120					125			
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys
		130				135					140				
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu
145					150					155					160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu
				165					170					175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His
			180					185					190		
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys
		195					200					205			
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys
	210					215					220				
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu
225					230					235					240
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile
				245					250					255	
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg
			260				265						270		
Leu	Val	Leu	Arg	Cys	Ser	Met	Asp	Asp	Ser	Ala	Gly	Pro	Arg	Ser	Pro

275		280		285
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser				
290		295		300
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala				
305		310		315 320
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys				
	325		330	335
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg				
	340		345	350
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr				
	355		360	365
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu				
	370		375	380

<210> 15

<211> 279

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Surfactant protein B precursor lacking the C-terminal propeptide

<400> 15

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr				
1		5		10 15
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys				
	20		25	30
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln				
	35		40	45
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly				
	50		55	60
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn				
	65		70	75 80
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu				
	85		90	95
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys				
	100		105	110
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln				
	115		120	125
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys				
	130		135	140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145 150 155 160
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
 165 170 175
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
 180 185 190
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
 210 215 220
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
 225 230 235 240
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
 245 250 255
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
 260 265 270
 Leu Val Leu Arg Cys Ser Met
 275

<210> 16
 <211> 79
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> PEPTIDE
 <222> (1) ... (79)
 <223> Mature surfactant protein B

<400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
 1 5 10 15
 Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
 20 25 30
 Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
 35 40 45
 Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
 50 55 60
 Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
 65 70 75

<210> 17
 <211> 431

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (431)

<223> Single-chain urokinase-plasminogen activator

<400> 17

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20 25 30

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65 70 75 80

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85 90 95

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His

260					265					270						
His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	
275					280					285						
Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	
290					295					300						
Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	
305					310					315					320	
Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	
					325					330					335	
Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	
					340					345					350	
Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	
355					360					365						
Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	
370					375					380						
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	
385					390					395					400	
Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	
					405					410					415	
Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu		
					420					425					430	

<210> 18

<211> 276

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (276)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 18

Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys
1				5					10					15	
Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile
			20				25						30		
Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly
			35				40						45		
Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val
			50			55							60		
Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr
65					70				75					80	

Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu
 85 90 95
 Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala
 100 105 110
 Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser
 115 120 125
 Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys
 130 135 140
 Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile
 145 150 155 160
 Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln
 165 170 175
 Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln
 180 185 190
 Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala
 195 200 205
 Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 210 215 220
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
 225 230 235 240
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
 245 250 255
 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn
 260 265 270
 Gly Leu Ala Leu
 275

<210> 19

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>

<221> PEPTIDE

<222> (282) ... (577)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr

1	5	10	15
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	20	25	30
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	35	40	45
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	50	55	60
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	65	70	80
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	85	90	95
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	100	105	110
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	115	120	125
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	130	135	140
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	145	150	160
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	165	170	175
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	180	185	190
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	195	200	205
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	210	215	220
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	225	230	240
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	245	250	255
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	260	265	270
Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu	275	280	285
Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys	290	295	300
Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala	305	310	320

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr	
1				5					10					15		
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys	
			20					25					30			
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln	
		35					40					45				
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly	
	50					55					60					
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn	
65					70					75					80	
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu	
				85					90					95		
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys	
			100					105					110			
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln	
		115					120					125				
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys	
		130				135					140					
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu	
145					150					155					160	
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu	
				165					170					175		
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His	
			180					185					190			
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	
		195				200						205				
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	
	210					215					220					
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu	
225					230					235					240	
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	
				245					250					255		
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	
			260					265					270			
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro	
		275					280					285				
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	

290	295	300
Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe 305 310 315 320		
Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys 325 330 335		
Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys 340 345 350		
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg 355 360 365		
Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu 370 375 380		
Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His 385 390 395 400		
Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala 405 410 415		
Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn 420 425 430		
Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu 435 440 445		
Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val 450 455 460		
Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser 465 470 475 480		
Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr 485 490 495		
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500 505 510		
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515 520 525		
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530 535 540		
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545 550 555		

<210> 21
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (197)

<223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His
50 55 60

Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln
65 70 75 80

Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile
85 90 95

Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala
100 105 110

Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro
115 120 125

Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe
130 135 140

Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys
145 150 155 160

Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly
165 170 175

Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val
180 185 190

Pro Leu Tyr Tyr Ile
195

<210> 22

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (58)

<223> Surfactant protein C precursor lacking the C-terminal propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu
50 55

<210> 23
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (35)
<223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val
1 5 10 15

Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu
20 25 30

Met Gly Leu
35

<210> 24
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (562)
<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35 40 45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50 55 60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80

Val	Pro	Val	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr		
				85					90					95			
Cys	Gln	Gln	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu		
			100					105					110				
Gly	Phe	Ala	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr		
		115					120					125					
Glu	Asp	Gln	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser		
	130					135					140						
Gly	Ala	Glu	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro		
145					150					160					165		
Tyr	Ser	Gly	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His		
			170						175					180			
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val		
			185					190					195				
Phe	Lys	Ala	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys		
		200					205					205					
Ser	Glu	Gly	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg		
	210					215					220						
Gly	Thr	His	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn		
225				230					235						240		
Ser	Met	Ile	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala		
			245					250						255			
Gln	Ala	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly		
		260					265						270				
Asp	Ala	Lys	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp		
		275					280					285					
Glu	Tyr	Cys	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr		
	290					295					300						
Ser	Gln	Pro	Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala		
305					310					315					320		
Ser	His	Pro	Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro		
			325						330					335			
Gly	Glu	Arg	Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile		
			340				345						350				
Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu		
		355					360					365					
Thr	Val	Ile	Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu		
	370					375					380						
Gln	Lys	Phe	Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp		
385					390					395					400		

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
 405 410 415
 Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
 420 425 430
 Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
 435 440 445
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
 450 455 460
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
 465 470 475 480
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
 485 490 495
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
 500 505 510
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
 515 520 525
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540
 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560

Arg Pro

<210> 25
 <211> 386
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1) ... (23)
 <223> Signal sequence of the surfactant protein B

<220>
 <221> PEPTIDE
 <222> (26) ... (104)
 <223> Mature surfactant protein B

<220>
 <221> PEPTIDE
 <222> (105) ... (380)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (381) ... (386)
 <223> Hexahistidin affinity tag

<400> 25

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr
1				5					10					15	
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Phe	Pro	Ile	Pro	Leu	Pro	Tyr
			20					25					30		
Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro
		35					40					45			
Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro
	50					55					60				
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val
65					70					75					80
Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys
				85					90					95	
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu
			100					105					110		
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile
		115					120					125			
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala
	130					135					140				
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly
145					150					155					160
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile
				165					170					175	
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg
			180					185					190		
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu
		195					200					205			
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp
	210					215					220				
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro
225					230					235					240
Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro
				245					250					255	
Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser
			260					265					270		
Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu
		275					280					285			
Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val
	290					295					300				

Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
 305 310 315 320
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
 325 330 335
 Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
 340 345 350
 Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
 355 360 365
 Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
 370 375 380
 His His
 385

<210> 26
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1) ... (20)
 <223> Signal sequence of the urokinase plasminogen activator

<220>
 <221> PEPTIDE
 <222> (23) ... (298)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (299) ... (377)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> PEPTIDE
 <222> (378) ... (383)
 <223> Hexahistidin affinity tag

<400> 26

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
 1 5 10 15

Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys
 20 25 30

Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly
 35 40 45

Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr
 50 55 60

Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu

65						70						75						80
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr			
				85					90					95				
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn			
			100					105					110					
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu			
		115					120					125						
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala			
	130					135					140							
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg			
145					150					155					160			
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe			
				165					170					175				
Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp			
			180					185					190					
Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser			
		195					200					205						
His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr			
	210					215					220							
Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln			
225					230					235					240			
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr			
			245					250						255				
Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys			
			260					265					270					
Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser			
		275					280					285						
His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	Phe	Pro	Ile	Pro	Leu	Pro			
	290					295					300							
Tyr	Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile			
305					310					315					320			
Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val			
			325						330					335				
Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser			
			340					345					350					
Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val			
		355					360					365						
Cys	Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	His	His	His	His	His	His	His			
370						375						380						

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